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FIG. 1A

1	TGGGAGCAGGCCTGGCCCCATCGGCTATGAGGGCGGGAAAGTGGGGCGGGTTGGGGAGCC	60
61	TCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGATAGGGCGAGGCT	120
121	GTGCTGTCCTTCAGAAGACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGTGG 1 M A S S I L K W V V	180 10
181	TCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGG 11 S H Q S C S R S S R S K P R D Q R E E A	240 30
241	CCGGGAGCAGCGACCTGAGCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGG 31 G S S D L S S R Q D A E N A E A K L R G	300 50
301	GCCTCCGGGGCAGTTGTGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGCAGC 51 L P G Q L V D I A C K V C Q A Y L G Q L	360 70
361	TGGAGCATGAGGACATCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCAGT 71 E H E D I D T S A D A V E D L T E A E W	420 90
421	GGGAGGACCTGACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTCATCTCCAATT 91 E D L T Q Q Y Y S L V H G D A F I S N S	480 110
481	CAAGAAATTACTTTCGCAGTGCAGGCCAGGCTCTGCTGAATAGAACATCGTCTGTGAACCCCTC 111 R N Y F S Q C Q A L L N R I T S V N P Q	540 130
541	AGACGGACATTGACGGGCTCCGAACATCTGGATTATAAAGCCCGGGCAAGTCCGGG 131 T D I D G L R N I W I I K P A A K S R G	600 150
601	GCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACC 151 R D I V C M D R V E E I L E L A A A D H	660 170
661	ACCCTCTTCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCA 171 P L S R D N K W V V Q K Y I E T P L L I	720 190
721	TCTGTGACACCAAGTTGACATCAGACAGTGGTTCTCGTCACGGACTGGAACCCCTGA 191 C D T K F D I R Q W F L V T D W N P L T	780 210
781	CCATCTGGTTCTACAAGGAGAGTTACTTGCAGGTTCTCAACTCAGCGCTCTCCCTGGACA 211 I W F Y K E S Y L R F S T Q R F S L D K	840 230

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FIG. 1B

841	AGCTGGACAGCGCCATCCACCTGTGCAACAACGCCGCCAGAAGTACCTGAAGAATGATG	900
231	L D S A I H L C N N A V Q K Y L K N D V	250
901	TGGGCCGCAGCCCCCTGCTGCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGT	960
251	G R S P L L P A H N M W T S T R F Q E Y	270
961	ACCTGCAGCGCCAGGGCCGTGGCGCCGTGGGGCAGCGTCATCTACCCGTCCATGAAGA	1020
271	L Q R Q G R G A V W G S V I Y P S M K K	290
1021	AGGCCATCGCCCACGCCATGAAGGTGGCCAGGACCACGTGGAGCCTCGCAAGAACAGCT	1080
291	A I A H A M K V A Q D H V E P R K N S F	310
1081	TTGAGCTCTACGGGCTGACTTCGTCCATTGGGAGGGACTTCAGGCCCTGGCTGATCGAGA	1140
311	E L Y G A D F V L G R D F R P W L I E I	330
1141	TCAATTCCAGCCCCACCATGCACCGTCCACGCCGGTCACGGCCAGCTGTGTGCACAGG	1200
331	N S S P T M H P S T P V T A Q L C A Q V	350
1201	TGCAGGAGGGACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGAACTTCGAGC	1260
351	Q E D T I K V A V D R S C D I G N F E L	370
1261	TCCTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCATTAGCGGGTCCGACCTCTGCGTGG	1320
371	L W R Q P V V E P P P F S G S D L C V A	390
1321	CGGGCGTCAGTGTGAGGGAGGCCAGGAGGCAGGTGCTGCCGTCTGCAACCTCAAGGCCT	1380
391	G V S V R R A R R Q V L P V C N L K A S	410
1381	CGGCCTCGCTGTTGGACGCGCAGCCGTGAAGGCACGGGGCCCTCGGCCATGCCAGACC	1440
411	A S L L D A Q P L K A R G P S A M P D P	430
1441	CTGCCCAGGGACCCCCATCACCAAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGG	1500
431	A Q G P P S P A L Q R D L G L K E E K G	450
1501	GGCTCCCCCTGGCCTTGTGGCACCCCTTAAGGGGGCAGCCGAGAGCGGTGGAGCCGCAC	1560
451	L P L A L L A P L R G A A E S G G A A Q	470
1561	AGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCCTGCCGCACG	1620
471	P T R T K A A G K V E L P A C P C R H V	490
1621	TGGACAGTCAGGCCAAACACCGGTGTCCCCGTAGCCCAGCCGCCAAAAGCTGGGATC	1680
491	D S Q A P N T G V P V A Q P A K S W D P	510

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FIG. 1C

1681	CAAACCAGCTAAATGCGCACCCGCTGGAGCCTGTGCTGCAGGGCTGAAGACAGCAGAGG	1740
511	N Q L N A H P L E P V L R G L K T A E G	530
1741	GCGCGCTGCGTCCGCCGCCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCA	1800
531	A L R P P G G K G S	541
1801	GGAGTACAGGTTGCAGCCACTCTCCAAGGGCGAATT C	1838

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FIG. 2

1	ATTGACGGGCTCCGAACATCTGGATTATAAGCCCGGCCAAGTCCGGGGCCGAGAC	60
1	I D G L R N I W I I K P A A K S R G R D	20
61	ATAGTGTGCATGGACCCTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCCTTT	120
21	I V C M D R V E E I L E L A A A D H P L	40
121	TCCAGGGACAACAAGTGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGAC	180
41	S R D N K W V V Q K Y I E T P L L I C D	60
181	ACCAAGTCGACATCAGACAGTGGTTCTCGTCACGGACTGGAACCCCCCTGACCATCTGG	240
61	T K F D I R Q W F L V T D W N P L T I W	80
241	TTCTACAAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGAC	300
81	F Y K E S Y L R F S T Q R F S L D K L D	100
301	AGGCCATCCACCTGTGCAACAAACGCCGCCAGAAGTACCTGAAGAATGATGTGGCCGC	360
101	S A I H L C N N A V Q K Y L K N D V G R	120
361	AGCCCCCTGCTGCCGCACACAAACATGTGGACCAGCACAGGTTCCAGGAGTACCTGCAG	420
121	S P L L P A H N M W T S T R F Q E Y L Q	140
421	CGCCAGGGCCGTGGCGCCGTGGGGCAGCGTCATCTACCGTCCATGAAGAAGGCCATC	480
141	R Q G R G A V W G S V I Y P S M K K A I	160
481	GCCCACGCCATGAAGGTGGCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTGAGCTC	540
161	A H A M K V A Q D H V E P R K N S F E L	180
541	TACGGGGCTGACTTCGTCTGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCC	600
181	Y G A D F V L G R D F R P W L I E I N S	200
601	AGCCCCACCATGCACCCGTCCAGGCCGTACGGCCAGCTGTGTGCACAGGTGCAGGAG	660
201	S P T M H P S T P V T A Q L C A Q V Q E	220
661	GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGG	720
221	D T I K V A V D R S C D I G N F E L L W	240
721	AGGCAG 726	
241	R Q 242	

FIG. 3A

	1	50
BGS-42	(1) -----MASSILKWWVSHQCSRSSRSKPRDQREEAGSSDLSSRQDAE	
TTL_PIG	(1) MYTFVVRDENSSVYAEVSRLLLATGHWKRLRRDNPRFNLGERNRLPFG	
TTLL_Hu	(1) -----MAGKVKWVTDIEKSVLINNFEKRGWVQVTENEDWNFYWMSV	
TTLH_Hu	(1) -----	
HOTTL	(1) -----	
	51	100
BGS-42	(43) NAEAKLRGIPGQLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTEAEWED	
TTL_PIG	(51) RLGHEPGLMQLVNYYRGADKLCRKASLVKLKITSPELAESCTWFPESTVI	
TTLL_Hu	(42) QTIRNVFSVEAGYRLSDDQIVNHFP--NHYELTRKDLMVKN--IKRYRKE	
TTLH_Hu	(1) -----MDIDKDLEAPLYLTPEGWSL	
HOTTL	(1) -----	
	101	150
BGS-42	(93) LTQQQYSIVHGDAFISNSRNYFSQCQALINRITSVNPQTIDGLRNWIIT	
TTL_PIG	(101) YPTNLKTPVAPAQNIGHPPIHSSRTDEREFFLTSYNKKKE-DGECKVWIA	
TTLL_Hu	(88) LEKEGSPLAEKDENGKYLYLDFVPVTYMLPADYNLFVEEFRKSPSSTWIM	
TTLH_Hu	(21) FLQRYYQVWHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEGDRNIWIV	
HOTTL	(1) -----MEGDRNFWIV	
	151	200
BGS-42	(143) KPAAKSRGRDIVCMDRVEETILEAAADHPISRDN-----KWVVQKYIERP	
TTL_PIG	(150) KSSAGAKGEGILLISSEATELLDFIDN-----QGQ-----VHVVIQKYLERP	
TTLL_Hu	(138) KPCGKAQGKGIFLTINKLSQTKKWSRDSKTSSFVQSNSKEAVVISLYINNP	
TTLH_Hu	(71) KPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDG-----KWVVQKYIERP	
HOTTL	(11) KPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDG-----KWVVQKYIERP	
	201	250
BGS-42	(188) LLIICD--TKFDITRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSA-	
TTL_PIG	(190) LLIEPGHRKFDITRSWVLVD--HQYNIYLYREGVILRTASEPMHTDNFQDKT	
TTLL_Hu	(188) LLIGGG--RKFDLRLVVLVSTYRPLRCYMYKLGFCRFCTVKYTIPSTSELDN	
TTLH_Hu	(116) LLIFG--TKFDLRLQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNS-	
HOTTL	(56) LLIFG--TKFDLRLQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNS-	
	251	300
BGS-42	(235) --IHLCNNNAVQKYLKNDVGRSPPLLPAHNMWTSSTRFQEYLQRQGRGAVWGS	
TTL_PIG	(238) --CHLTNHCIQKEYSKNYGKYE--E-GNEMFFEEFNQYLTSA-NITIES	
TTLL_Hu	(236) MFVHLTNVAIQKHGEDYNHIH---G-GKWTIVSNLRLYLESTR-GKEVTS	
TTLH_Hu	(163) --VHLCNNSIQKHLENSCHRHPLLPDNMWSSQRFOAHLQEMGAPNAWST	
HOTTL	(103) --VHLCNNSIQKHLENSCHRHPLLPDNMWSSQRFOAHLQEMGAPNAWST	
	301	350
BGS-42	(283) VIYPSMKKAIAHAMKVAQDHVEPRKN---SFELYGADFVLGRDFRPWLIE	
TTL_PIG	(282) SILLQTKHIIIRSCLLSSVEPAISTRHLPYQSFQLFGFDFMVDEDLKVWLIE	
TTLL_Hu	(280) KLFDEIHWIIIVQSLKAVAPVMNNDKH---CFECYGYDI I IDDKLKPWLIE	
TTLH_Hu	(211) IIIVPGMKDAVIHALOTSQDTVOCRKA---SFELYGADFVGEDFOPWLIE	
HOTTL	(151) IIIVPGMKDAVIHALOTSQDTVOCRKA---SFELYGADFVGEDFOPWLIE	

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FIG. 3B

BGS-42 (330)	INSSPTMHPSTPVTAQLCAQVQE DTI KVAVD -----RS CDIG	351 400
TTL_PIG (332)	VNG-----APACAQKLYAEICQGIVDIAIAS-----	
TTLL_Hu (327)	VNASPSLTSS STANDRIL KYNLINDTLNIA VPNGEIPDCKWNKSPPK EVLG	
TTLH_Hu (258)	INASPTMAPSTA TARL CAGVQADTLRVVIDR -----MLDRNCDTG	
HOTTL (198)	INASPTMAPSTA TARL CAGVQADTLRVVIDR -----MLDRNCDTG	
BGS-42 (367)	NFELLWRQPVVE PPPF SGSDLCVAGVSVRRARRQVLPVCNLKASASLLDA	401 450
TTL_PIG (358)	V PPP D AEQQQQ -----OPPPAAFIKL-----	
TTLL_Hu (377)	NYE I LYDEELAQGDGADRELRSRQGQSLGPRAGR-----SRDSGRAVLT	
TTLH_Hu (299)	A FELI IYKQPVTTSPASTPRPSC SCL LP MYS DTRAR-----SSDDSTASW	
HOTTL (239)	A FELI IYKQPVTTSPASTPRPSC SCL LP MYS DTRAR-----SSDDSTASW	
BGS-42 (417)	QPL KARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLA PLRGAAESG	451 500
TTL_PIG (380)	-----	
TTLL_Hu (422)	WK-----	
TTLH_Hu (341)	WALRPCR PQARP -----	
HOTTL (281)	WALRPCR PQARP -----	
BGS-42 (467)	GAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAH	501 550
TTL_PIG (380)	-----	
TTLL_Hu (424)	-----	
TTLH_Hu (353)	-----	
HOTTL (293)	-----	
BGS-42 (517)	PLEPVLRGLKTAEGALR PPP GGKGS	551 575
TTL_PIG (380)	-----	
TTLL_Hu (424)	-----	
TTLH_Hu (353)	-----	
HOTTL (293)	-----	

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FIG. 4

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FIG. 5A**BGS-42 – Clone A**

TGGGAGCAGGCCTGGGCCCATCGGCTATGAGGGCGGAAGTGGGGCGGTTGG
 GGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTGGACAGAT
 AGGGCGAGGCTGTGCTGCTTCAAGAACACTCCGGCGACCATGGCATCCAGC
 ATCCTCAAGTGGTGGTCAGCCACCAAGCTGCAGCAGGAGCAGCAGAAGCAAG
 CCCAGGGACCAGAGGGAGGAGGCCGGAGCAGCAGCAGCAGGCAAGA
 TGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCGGGAGCTTGAGGACATCGA
 CGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCAGTGGAGGACATCGA
 CACGTCAAGCAGATGCCGTGGAGGACCTCACTGAGGCCAGTGGAGGAGGACCTGAC
 CCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTCATCTCCAATTCAAGAAATT
 ACTTTCGCAGTGCCAGGCTTGCTGAATAGAATCACGTCTGTGAACCCCTCAGAC
 GGACATTGACGGGCTCCGGAACATCTGGATTATAAGCCCGGGCCAAGTCCCG
 GGGCCGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTC
 ATCTGTGACACCAAGTCGACATCAGACAGTGGTCTCGTCACGGACTGGAACC
 CCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCAGGCTCTCAACTCAGCGCTT
 CTCCCTGGACAAGCTGGACAGCGCCATCCACCTGTGCAACAAACACCGTCCAGAA
 GTACACTGAAGAATGATGTGGGCCGAGCCCCCTGCTGCCGACACAAACATGTG
 GACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTG
 GGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATGCCACGCCATGAAGGT
 GGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTGAGCTCTACGGGGCTGA
 CTTCGTCCTGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCC
 ACCATGCACCCGTCCACGCCGGTCACGCCAGCTGTGACATCGGCAACTCGAGCTC
 GACACCATCAAGGTGGCCGTGGTGGAGCCGGCCATTCAAGGGTCCGACCTCTGCG
 CTGTGGAGGCAGCCGGTGGTGGAGCCGGCCATTCAAGGGTCCGACCTCTGCG
 TGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGGCCAGGTGCTGCCGTCTGCAACC
 TCAAGGGCTCGCCTCGCTGTTGGACCGCAGCCGCTGAAGGCACGGGGCCCT
 CGGCCATGCCAGACCCGTGCCAGGGACCCCCATCACCAGCTCCAGGGGACTT
 GGGACTGAAGGAAGAGAACAGGGCTCCCCCTGGCTTGGACCCCTTAAGGGG
 GGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCGCACCAAAGCTGCTGGAA
 GGTGGAGCTCCGGCTGCCCTGTCGCCACGTGGACAGTCAGGCCAAACAC
 CGGTGTCCCCGTAGCCAGCCGCCAAAAGCTGGATCAAACCAAGCTAAATGA
 GCACCCGCTGGAGCCTGTGCTGCCAGGGACCTGAAGACAGCAGAGGGCGCTGCG
 TCCGCCGCCGGAGGAAAAGGTTATGACAGCGTCAGATTCTCTGCAGCAGGAG
 TACAGGTTGCAGCCACTCTCCGCCAACATTGAATACTGTCTTCCACCATTTGT
 CTTGCTGTGGCTCTGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGAG
 CTGTCAGTTCTATGCCCCAGCTTGTGAGTGTCAATTGATTTTACTTATTCAACC
 TGGAATTGAATGTCAAAAAAAAAAAAAA (SEQ ID NO:9)

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FIG. 5B**BGS-42 – Clone B**

GTAGCAGCGTGGGAAGAAGGAGTTCTGGAAAGACTTCGGCGCACCATGGCATC
CAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAG
CAAGCCCAGGGACCAGAGGGAGGAGGCCGGAGCAGCAGCTGAGCAGCAGGC
AAGATGCTGAAAATGCTGAGGCCAAAGCTCAGGGGCCTCCGGGGCAGCTGTGG
ACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACA
TCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCAGTGGAGGACC
TGACCCAGCAGTACTACTCCCTCGTTCATGCCAGGCTCTGCTGAATAGAACG
TCTGTGAACCCTCAGACGGACATTGACGGCTCCGGAACATCTGGATTATAAAGC
CCGGGCCAAGTCCCAGGGCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGA
TCCTGGAGCTGGCAGCTGCAGACCACCCCTTTCCAGGGACAACAAGTGGGTGG
CCAGAAGTACATCGAGACGCCGTGCTCATCTGTGACACCAAGTTCGACATCAG
ACAGTGGTCCCTCGTCACGGACTGGAACCCCCCTGACCATCTGGTTCTACAAGGAG
AGTTACTTGCAGGTTCTCAACTCAGCGCTCTCCCTGGACAAGCTGGACAGGCCA
TCCACCTGTGCAACAAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCA
GCCCGCTGCTGCCGCACACAACATGTGGACCAGCACCGGTTCCAGGAGTACCT
GCAGGCCAGGGCGTGGCGCGTGTGGGGCAGCGTCATCTACCCGTCCATGAA
GAAGGCCATGCCACGCCATGAAGGTGGCCAGGACCACTGGAGCCTCGCAA
GAACAGCTTGAGCTCTACGGGCTGACTCGTCCCTGGAGGGACTTCAGGCC
TGGCTGATCGAGATCAATTCCAGCCCCACCATGCAACCGTCCACGCCGTACGG
CCCAAGCTGTGTCACAGGTGCAGGAGGACACCATCAAGGTGGCGTGGACCGCA
GCTGTGACATCGCAACTTCGAGCTCCTGTGGAGCCGGTGGTTGAGCCCCCCA
TTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGG
CAGGTGCTGCCGTCTGCAACCTCAAGGCCCTGGCCTCGCTGTTGGACGCCAGC
CGCTGAAGGCACGGGCCCTCGGCCATGCCAGACCCCTGCCAGGGACCCCCAT
CACCAAGCTCTCCAGCGGACTTGGACTGAAGGAAGAGAAGGGCTCCCCCTGG
CCTTGCTGGCACCCCTTAAGGGGGCAGCGAGAGCGGTGGAGGCCACAGCCA
CCCGCACCAAAGCTGGAAAGGTGGAGCTCCCGGCCCTGCCACGT
GGACAGTCAGGGCCAAACACCGGTGCCCCGTAGCCCAGCCGCCAAAGCTG
GGATCCAAACCAAGCTAAATGAGCACCCGCTGGAGCCTGTGCTGCCAGGAGCCTGAA
GACAGCAGAGGGCGCGTGCCTGCCGCCGGAGGAAAAGGTTCATGACAGCG
TCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCCACTCTCCGCCAACATTGA
ATACGTCTTCCACCATCTTGTCTTGCTGTGGCTCTGGAAAATCAGCAGAGTC
AGCCATCACTCTCAAGGGAGCTGTCAGTTCTATCTGCCAGCTTTGAGTGTTC
AATTGATTTACTTATTCAACCTGGAATTGAATGTCAAAAAAAAAAAAAAAA
AAAAAAAAA (SEQ ID NO:10)

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FIG. 5C**BGS-42 – Clone C**

CCCAGGACTCTGGTCTAAGGCCGTGCCAGAACATCACTCGTGCCCACCCACCC
 CCAGCACCCCTGTGCCCTTGCTCTGTCTCTGGGTGAATCCGGGCCCCAGAA
 GCTCCCTCCTCAGGGCACAGAGGCCAAGATGGGGCTGACTGGGGCTGCCACC
 GGGCTTGGGTGCTGAGGGGGCTGTGGGACCCCAGGGGAAGAGGTGCCGCTCCC
 CCCAGCACCGGGCACTCCCCGCCTCCCCCGGCCTCCAGCCCTGCACAAAGCAGC
 TTGCCACACCCTCCCACCAAGGCCAGGGCTGAGGCCAGGACGCAGGG
 TGTGGGACCCCTGCTGAGGGAGGGTCCCGGAAGAGGGCTCCCTGGCACAGA
 GGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAGGT
 GCAGGACAAGGTTCCCTCCGCACCTAATACCCCAAGGGTCAGGCCAGGCCAGC
 GCTGCTAGTGGCAACATGGCCCTCAAAGACCCCGTGTGCAGAGCCAGTCAGC
 GTGCGCTGTGTTCTGGGGCCAGCCACTTTTCCTTAACGGGTGACAAACC
 AGACATCGGGGTGCGGGGACTTCACGATATGCCCTCTAATGGCGCGTGTACCT
 CGCGTGTGGTGGCAGTGCTGGCATGTGGCTGCCTCCGGGCCCTGCAGCCGCT
 CCTCCCTCTCCTGGGTCTGAGGTGTGGACACCCCTGTGGCCCTTGGGGCCT
 GGAGGGAGCCCCAGTGCCACGCCCTCCACTGCCTCAAGGATGCGTGTAGCCTGGCCTG
 CACATCCATGCTCCCACCGGCTGGAGGGGGTTCTGGGGCCCTGGGGGACCGT
 ATATCTGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTGCCTTCAG
 CCAGGCAAGTCTGAGGTGGACGGCCCTCCTCGCTTGTGAGCGAGGCAGAGCT
 GAGCTGAGCTGCCCTCCTGCCCTAACACGCCACTGTCTCTGGAGATCGGCTGTG
 CGTGAACATGCGGAGCCTGCCCTGGTACGTCCCAGCAACCCGACTCCTCTTC
 CCACGCTGCTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCTGGTAAG
 TGAGGAGACGGCAGAGGGCCCCAGTGTGTCAAGCAGAGAGGGCTTAGAAAGAT
 CCCCCTGGTGCTGAGACAGACTGATGGGCAGGGTCTGAGGATAGAGGACCGGG
 GAGAGGCCTCCATGGTCATGGCATGGCAGTACAGAGGCCAGGGGCCAGGGGGGG
 GGGAGGGCGGGCAGTCAAGGAGTGTGGTTCTGTGCTAGGCTGTGGACAGCG
 CGGCGAGCAGCTGGGCAAGGCCGGCTCCGTGGTCGGAGGCCAGGGTGCAGC
 TGGACGCCGAGTCACAGAGACACTGCAGGGAGAACGGCAGGCAGACTGGGG
 GTGTGGGAGCAGGCCTGGCCCCATCGCTATGAGGGCGGGAAAGTGGGGCGGG
 TGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCTGGCTCGGACA
 GATAGGGCGAGGCTGTGCTGTCTTCAAGAACACTCCGGCGCACCATGGCATCC
 AGCATCCTCAAGTGGGTGGTCAGCCACCAAGAGCTGCAGGAGCAGCAGCAGAAGC
 AAGCCCAGGGACCAGAGGGAGGAGGCCGGAGCAGGACCTGAGCAGCAGGCA
 AGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCGGGAGCAGCTGTGGA
 CATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACAT
 CGACACGTCAAGCAGATGCCGTGGAGGACCTCACTGAGGCCAGTGGGAGGACCT
 GACCCAGCAGTACTACTCCCTCGTTATGGCGATGCTTCTGATCTCCAATTCAAGA
 AATTACTTTCGCAAGTGCAGGCCAGGCTCTGTAATAGAACATCACGCTGTGAACCC
 AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAGCCCGGGCCAAGT
 CCCGGGCCAGGGACAACAAGTGGGTGGTCAGAAGTACATCGAGACGCCGCT
 GCTCATCTGTGACACCAAGTTGACATCAGACAGTGGTTCTCGTCACGGACTGG
 AACCCCCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCAGGTTCTCAACTCAGC
 GCTTCTCCCTGGACAAG

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FIG. 5C (CONT.)

CTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAA
GAATGATGTGGGCCGCAGCCCCCTGCTGCCGCACACAACATGTGGACCAGCAC
CAGGTTCCAGGAGTACCTGCAGGCCAGGGCCGTGGCGCCGTGGGGCAGCGT
CATCTACCCGTCCATGAAGAACAGGCCATGCCACGCCATGAAGGTGGCCCAGGA
CCACGTGGAGCCTCGCAAGAACAGCTTGAGCTCTACGGGGCTGACTCGTCCTT
GGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCATGCAC
CCGTCCACGCCGGTCACGGCCCAGCTGTGCACAGGTGCAGGAGGACACCATC
AAGGTGCCGTGGACCCAGCTGTGACATCGCAACTTCAGCTCCTGTGGAGG
CAGCCGGTGGTTGAGCCGGCCCCATTAGCGGGTCCGACCTCTCGTGGCGGGCG
TCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCGTCTGCAACCTCAAGGCCT
CGGCCTCGCTGTTGACCGCAGCCGCTGAAGGCACGGGGCCCTCGGCCATGC
CAGACCCCTGCCAGGGACCCCCATCACCAGCTCCAGCGGGACTTGGGACTG
AGGAAGAGAACGGGGCTCCCCCTGGCCTTGCTGGCACCTTAAGGGGGCAGCCG
AGAGCGGTGGAGCCGACAGCCCACCCGACCAAAGCTGCTGGGAAGGTGGAGC
TCCCAGGGCTGCCCTGTCGCCACGTGGACAGTCAGGCCAAACACCCGGTGTCCC
CGTAGCCCAGCCGCCAAAAGCTGGATCCAACACCAGCTAAATGAGCACCCGCT
GGAGCCTGTGCTGCCAGGGAGCCTGAAGACAGCAGAGGGCGCGCTCGTCCGCC
CGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTG
CAGCCACTCTCCGCCAACATTGAATACTGCTTCCACCATCTTGTCTTGCTGT
GGCTCTGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGAGCTGTCAGT
TCTATCTGCCAGCTTTGAGTGTCAATTGATTTACTTATTCAACCTGGAATT
GAATGTCAAAAAAAAAAAAAAA (SEQ ID NO:11)

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FIG. 6A

1	GTCTAAGGCCGTGGCCAGAATCACTCGGTGCCACCCCACCCCCAGCACCCCTGTGCCCT	60
61	TTGCTCTGTGTCTCTGGGTGAATCCGGGGCCCCAGAACGCTCCCTCCTCAGGGCACAGAGG	120
121	CCAAAGATGGGGCTGACTGGGGCTGCCACCGGGCTTGGGTGCTGAGGGGGCTGTGGGA	180
181	CCCCAGGGGAAGAGGTGCCGCTCCCCCAGCACCGGGCACTCCCCGCCTCCCCGCCCT	240
241	CCAGCCCTGCACAAAGCAGCTGCCACACCCCTCCACCAAGGCCAGGGCTGAGGCCTG	300
301	CCCAGGACGCAGGGTGTGGGACCCCTGCTGAGGGAGGGTCCCGGAAGAGGGGGCTTCCT	360
361	GGCACAGAGGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAG	420
421	GTGCAGGACAAGGTTCCCTTCCGCACCTAATACCCAGGGTCAGGCCAGCGCCAGCGCTG	480
481	CTAGTGGCAACATGGCCCTTCAAAGACCCCGTGTGCAGGCCAGTCAGCGTGCCTGTG	540
541	TTTCTGGGGGCCAGCCACTTTTCTTAACGGGGTGACAAACCAGACATCGGGGTGCG	600
601	GGGACTTCACGATATGCCTCTTAATGGCGCGTGTACCTCGCGTGTGGTGGCAGTGCT	660
661	GGGCATGTGGCTGCGTTCCGGCCCTGCAGCCGCTCCCTCTCCCTGGGGTCTGAGGTG	720
721	TGGGACACCCCTGTGGCCGTTGGGGCCTGGAGGGAGCCCACTGCCACGCCCTCCACTGCCTCAAGG	780
781	TGCCCTCAGCTGCAGCCTCCCCATTCCCTGGGGCTGCCACGCCCTCCACTGCCTCAAGG	840
841	ATGCGTCTGAGCCTGGCCTGCACATCCATGCTCCCACCGGCTGGAGGGGGTGTCTGGG	900
901	CCCTGGGGACCGTATATCTGGGAGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGT	960
961	CCCCATGCCAGGCAAGTCTGAGGTGGACGCCGTCCTCGCCTTGAGCGAGGCAGAG	1020
1021	CTGAGCTGAGCTGCCCTCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTGCGT	1080
1081	GAACATGCCAGGCTGCCCTGGTACGTCCCAGCAACCCGACTCCTTCTCCCACGCTG	1140

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FIG. 6B

1141	CTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTCCTGGTAAGTGAGGAGACGGCAG	1200
1201	AGGGCCCCAGTGTGTCAGCAGAGAGGCTTAGAAAGATCCCCCTGGTGTGAGACAGA	1260
1261	CTGATGGGGCAGGGTCTGAGGATAGAGGACCGGGAGAGGCCTCCATGGTCATGGTCAT	1320
1321	GGCAGTACAGAGGCCAGGGCCCCGGGAGGGAGGGCGGGCAGTCAGGAGTGTGTGGTTC	1380
1381	TGTGCTAGGTTGTGGACAGCGCGCGAGCAGCTGGCAAGGCCGGCTCCGTGGTCGGA	1440
1441	GGCGAGGGGTGCAGCTGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGC	1500
1501	AGACTGGGGTGTGGAGCAGGCCTGGCCCATCGGCTATGAGGGCGGGAAAGTGGGCG	1560
1561	GGTTGGGAGCCTCCGTGGCCCTGGCCCATCTCCAGTCAGCTGGCTGGACAGA	1620
1621	TAGGGCGAGGCTGTGCTGTCCTTCAGAGTAGCAGCGTGGAAAGAAGGAGTTCTGGAAG	1680
1681	ACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGTGGTCAGCCACCAGAGCTGCA	1740
1	M A S S I L K W V V S H Q S C S	16
1741	GCAGGAGCAGCAGAACAGCAAGCCAGGGACCAGAGGGAGGGAGGCCGGAGCAGCGACCTGA	1800
17	R S S R S K P R D Q R E E A G S S D L S	36
1801	GCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGCCTCCGGGCAGCTTG	1860
37	S R Q D A E N A E A K L R G L P G Q L V	56
1861	TGGACATCGCGTCAAGGTGTGCCAGGCCTACCTGGGAGCTGGAGCATGAGGACATCG	1920
57	D I A C K V C Q A Y L G Q L E H E D I D	76
1921	ACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCAGTGGAGGACCTGACCCAGC	1980
77	T S A D A V E D L T E A E W E D L T Q Q	96
1981	AGTACTACTCCCTCGTTCATGGCGATGCTTCATCTCCAATTCAAGAAATTACTTTCGC	2040
97	Y Y S L V H G D A F I S N S R N Y F S Q	116
2041	AGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCTCAGACGGACATTGACGGC	2100
117	C Q A L L N R I T S V N P Q T D I D G L	136

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FIG. 6C

2101	TCCGGAACATCTGGATTATAAGCCCGCGGCCAAGTCCCAGGGCCGAGACATAGTGTGCA	2160
137	R N I W I I K P A A K S R G R D I V C M	156
2161	TGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCCTTTCCAGGGACA	2220
157	D R V E E I L E L A A A D H P L S R D N	176
2221	ACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGTGCTCATCTGTGACACCAAGTCG	2280
177	K W V V Q K Y I E T P L L I C D T K F D	196
2281	ACATCAGACAGTGGTCTCGTCACGGACTGGAACCCCTGACCATCTGGTTCTACAAGG	2340
197	I R Q W F L V T D W N P L T I W F Y K E	216
2341	AGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCATCC	2400
217	S Y L R F S T Q R F S L D K L D S A I H	236
2401	ACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCAGCCCCCTGC	2460
237	L C N N A V Q K Y L K N D V G R S P L L	256
2461	TGCCCGCACACAACATGTGGACCAGCACAGGTTCCAGGAGTACCTGCAGCGCCAGGGCC	2520
257	P A H N M W T S T R F Q E Y L Q R Q G R	276
2521	GTGGCGCCGTGTGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATGCCAACGCCA	2580
277	G A V W G S V I Y P S M K K A I A H A M	296
2581	TGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTGAGCTCTACGGGCTG	2640
297	K V A Q D H V E P R K N S F E L Y G A D	316
2641	ACTTCGTCCCTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCA	2700
317	F V L G R D F R P W L I E I N S S P T M	336
2701	TGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTCACAGGTGCAGGAGGACACCATCA	2760
337	H P S T P V T A Q L C A Q V Q E D T I K	356
2761	AGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCTGTGGAGGCAGCCGG	2820
357	V A V D R S C D I G N F E L L W R Q P V	376
2821	TGGTTGAGCCGCCATTCAAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGA	2880
377	V E P P P F S G S D L C V A G V S V R R	396
2881	GAGCCAGGAGGCAGGTGCTGCCGTCTGCAACCTCAAGGCCTGGCCTCGCTGTTGGACG	2940
397	A R R Q V L P V C N L K A S A S L L D A	416

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FIG. 6D

2941	CGCAGCCGCTGAAGGCACGGGGCCCTCGGCCATGCCAGACCCCTGCCAGGGACCCCAT	3000
417	Q P L K A R G P S A M P D P A Q G P P S	436
3001	CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGC	3060
437	P A L Q R D L G L K E E K G L P L A L L	456
3061	TGGCACCCCTTAAGGGGGCAGCCGAGAGCGGTGGAGGCCACAGCCCACCCGCACCAAAG	3120
457	A P L R G A A E S G G A A Q P T R T K A	476
3121	CTGCTGGGAAGGTGGAGCTCCCGCCTGCCCTGTCGCCACGTGGACAGTCAGGCCCAA	3180
477	A G K V E L P A C P C R H V D S Q A P N	496
3181	ACACCGGTGTCCCCTAGCCCAGCCGAAAAGCTGGATCAAACCAGCTAAATGAGC	3240
497	T G V P V A Q P A K S W D P N Q L N E H	516
3241	ACCCGCTGGAGCCTGTGCTGCCAGCCTGAAGACAGCAGAGGGCGCTCGTCCGCCGC	3300
517	P L E P V L R S L K T A E G A L R P P P	536
3301	CCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCC	3360
537	G G K G S	541
3361	ACTCTCCGCCAACATTGAATACGTCTTCCACCATCTTGTCTTGCTGGCTCTGGG	3420
3421	AAAATCAGCAGAGTCAGCCATCACTCTCAAGGGAGCTGTCAGTTCTATCTGCCAGCTT	3480
3481	TTGAGTGTCAATTGATTTACTTATTCAACCTGGAATTGAATGTCAAAAAAAAAAA	3540
3541	AAAAAAAAAAAAAA	3554

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FIG. 7A

-2057	tgcctgcagcagagccggctggatcctcacgctgcacgccattgtcctctgatggtt	-1998
-1997	gcctcaactccatccatcctggctggtgt <u>qaaccttqaatqctggcatcaataaaqact</u>	-1938
-1937	<u>ttttcttgc</u> agtctaqqtqqtaaaaatqaqatqccqtaacctcctctqgaccatcaa	-1878
-1877	<u>gagg</u> gacatcattqactatcacacqctqacacctacqaccqatqctgaaccactacqaaa	-1818
-1817	<u>aca</u> qcctccttcaccaccaaqqtqagccqccqccqcttqaqcqttggcqggqacccqgcaa	-1758
-1757	<u>qqqtqqtqqqq</u> aggagcttctgcagccattaggaccctcggtggctggtcagtggccac	-1698
-1697	cagtcacccctgggtgcattccaggactcctggcttaaggccgtggccagaatcactcg	-1638
-1637	gtgcccaccccacccccagcacccctgtgcctttgtctgtctctgggtgaatccgg	-1578
-1577	ggccccagaagctccctcctcaggcacagaggccaaagatgggctgactggggctgc	-1518
-1517	caccgggcttgggtgctgaggggctgtgggaccggcaggggaaagaggtgccgctcccc	-1458
-1457	cagcacccggcactccccgcctccccggcctccagccctgcacaaagcagcttgcac	-1398
-1397	acccttcccaccaaggcccagggtgaggcctgcccaggacgcagggtgtgggaccctg	-1338
-1337	ctgagggaggggtccggaagagggctccctggcacagaggcccttcagcaggcca	-1278
-1277	ggtgcggctgcctcagcacagtgtggggcggagggtgcaggacaagg <u>ttccctccgcacc</u>	-1218
-1217	<u>taata</u> ccccaggqtcaaggccaggccatqctagttggcaacatggcccttcaaaga	-1158
-1157	<u>cccc</u> gtgtgcagaggccaggcgtcaqgtgcgtgttttctqqqqqccacccactttcc	-1098
-1097	<u>ttaaca</u> qggqtacaaaccaqacatcgggtacgggacttcacqatatqcctctaatq	-1038
-1037	<u>gcgcgt</u> qctacccgcgtgtggcggaggactqggcatqtggctqcqttccggccctg	-978
-977	<u>ca</u> gcccqctcccttcctgggtctqagggtgtggacaccctgtggcccgtttggggg	-918
-917	cctggagggagcccaggcgcaccgcctcggtgcctcagctgcagcctccccattcc	-858

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FIG. 7B

-857 ctggggcctgccacgcgcctccactgcctcaaggatgcgtctgagcctggcctgcacatcc -798

-797 atgctcccaccggctggaggggggtgttctggggcctgggggaccgtataatctggggagg -738

-737 gggagggatccgcgcctaaqqqqtqctqtqgtqgtqcccataqccaggcaagtctqaggta -678

-677 acqqccccqtcctcqcccttqtaqcgaggcaqagctqagctqagctqcccctctqccta -618

-617 cacqccactqtctctqqaqatcqqqctqtqcgtqaacatqcqgagcctqccctqgtacqt -558

-557 cccqgccaaccccqactccttcttccacqctqctacagcctctqcaccqagqagtqagca -498

-497 qcaaggqatttcctqqqtaqgtqaqqqacqggcagaggccccagtgctgtcagcagagagg -438

-437 cttctagaaaagatccccctggtgctgagacagactgatggggcagggtctgaggatagag -378

-377 gaccggggagaggcctccatggcatggcatggcagttacagaggccagggccccggg -318

-317 agggagggcgggcagtcaaggagtgtgtggttctgtgctaggctgtggacagcgcggcg -258

-257 agcagctgggcaaggccggctccgtggcggaggccgaggggtgcagctggacggccgc -198

-197 agtcacagagacactgcagggagaagggcaggcagactgggggtgtggagcaggctgg -138

-137 gccccatcggtatgggcgggaagtggggcgggtgggagacccgtggccctggcc -78

-77 ccatctccagtcggcgtggcggcggatggcggatggcggcggcggcggcggcggcggc -18

-17 aagacttccggcgcaccatggcatccgcacatccctcaagtgggtggtcagccaccagact 42
1 M A S S I L K W V V S H Q S C 15

43 gcagcaggaggcagcagaagcaagccgcaggaccagaggaggaggccgggagcagcggacc 102
16 S R S S R S K P R D Q R E E A G S S D L 35

103 tgagcaggcaggcaagggtgcgtggccggggcaggcaggcagtgcgcaggccaccagagctgg 162
36 S S R Q G A L G R G R A V P G H Q S S G 55

163 ggccctccacaggggccctccc 183
56 P P Q G P S 61

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FIG. 8

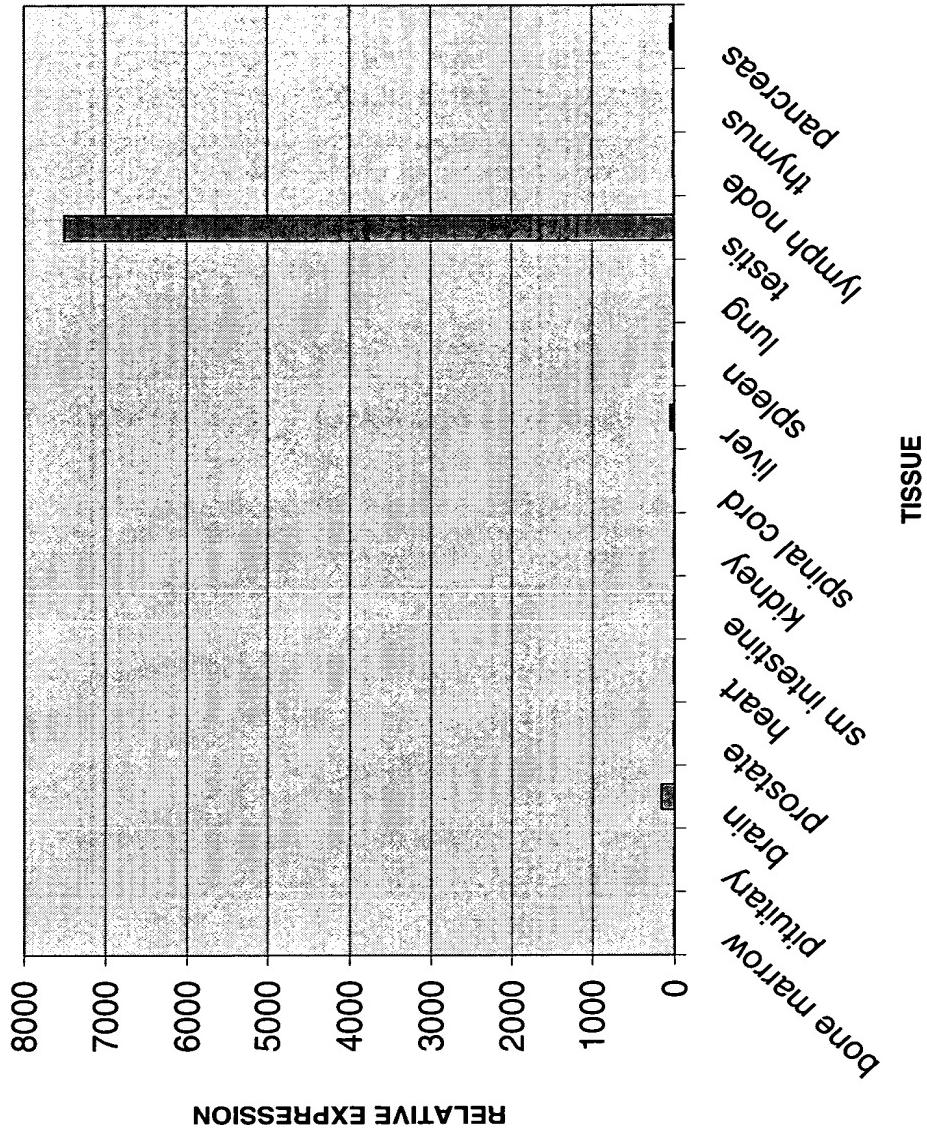


FIG. 9

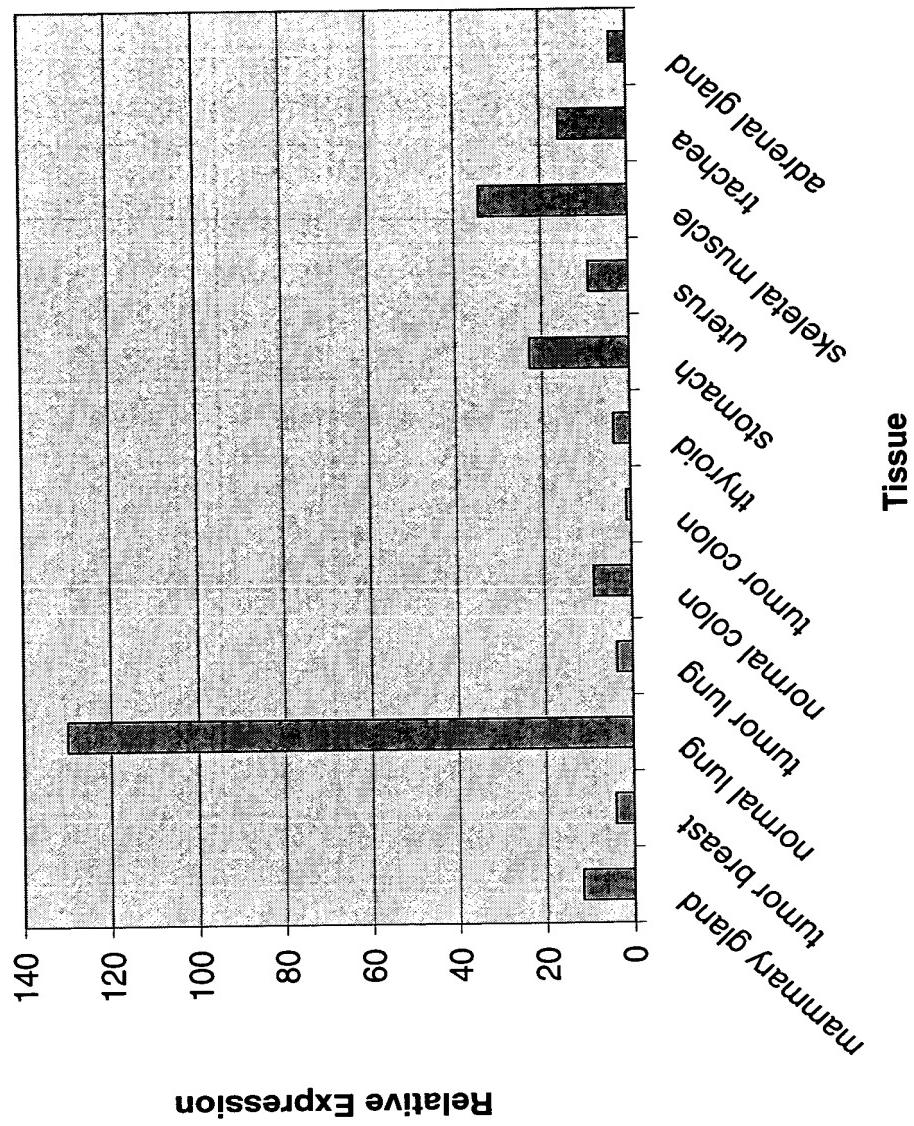
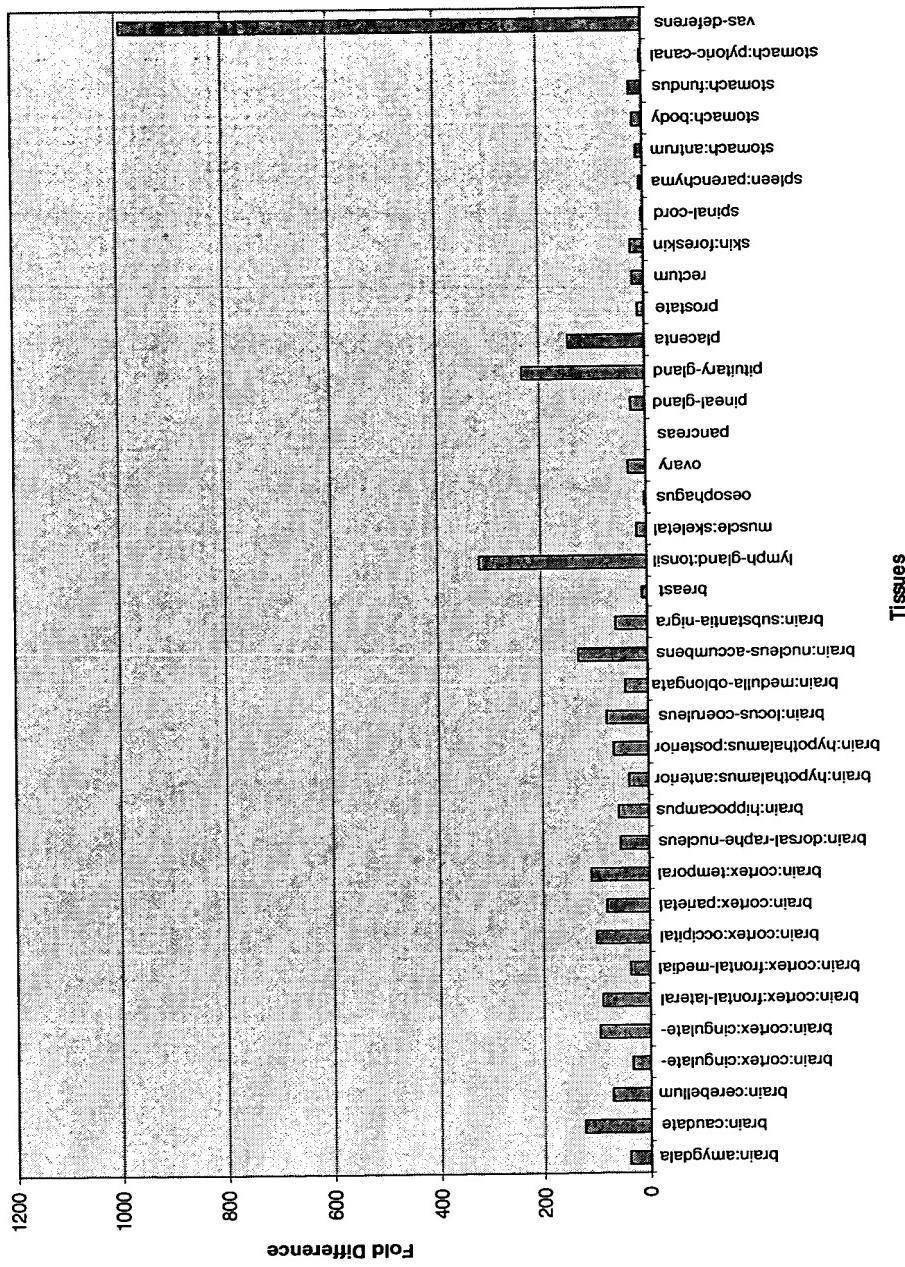


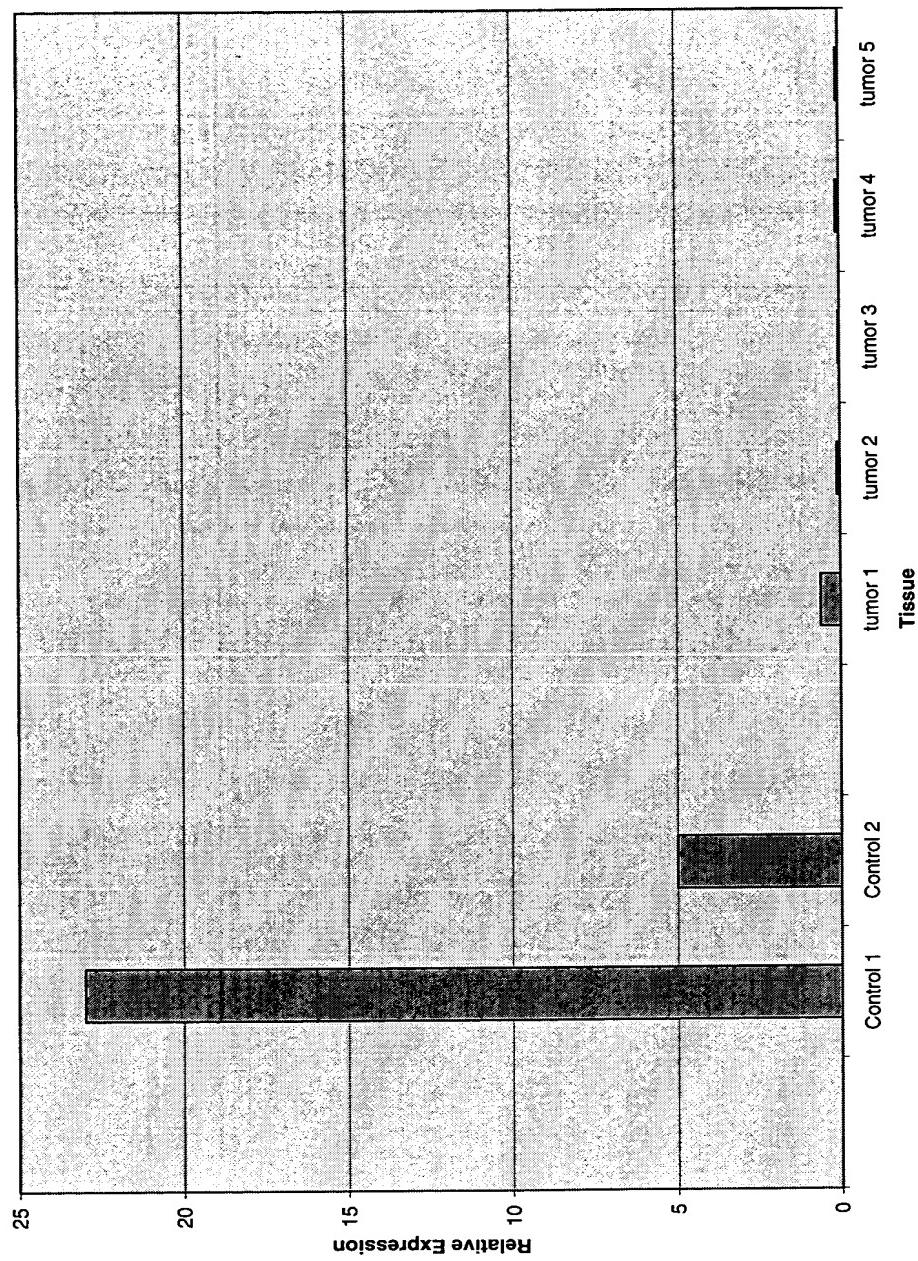
FIG. 10



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FIG. 11



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Protein	Genbank ID	Identities	Similarities
Human HOTTL protein	gi 6683745	57.5%	65.5%
Pig tubulin--tyrosine ligase protein (TTL)	gi 423218	29.4%	40.0%
Human tubulin tyrosine ligase-like protein (TTLH_HUMAN)	gi 20455371	53.3%	61.4%
Human tubulin tyrosine ligase-like protein (TTLL_HUMAN)	gi 20455347	27.4%	38.4%